WEST Search History

DATE: Tuesday, December 10, 2002

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,PGPB; PLUR=YES; OP=ADJ		
L11	L10 and l7	10	L11
L10	L9 and (dna or cdna or nucleic acid or polynucleotide)	18	L10
L9	L8 and (coryneformbacter? Or corynebacteria or corynebacteria glutamicum)	18	L9
L8	SecD or secf	90	L8
L7	L6 or l5 or l4 or l3 or l2 or l1	26644	L7
L6	(((536/23.1)!.CCLS.))	7951	L6
L5	(((530/350)!.CCLS.))	8278	L5
L4	(((435/320.1)!.CCLS.))	14154	L4
L3	(((435/252.32)!.CCLS.))	117	L3
L2	(((435/252.3)!.CCLS.))	6265	L2
L1	((435/69.1)!.CCLS.)	9966	L1

END OF SEARCH HISTORY

WEST

Generate Collection | Print

Search Results - Record(s) 1 through 10 of 10 returned.

1. Document ID: US 20020172999 A1

L11: Entry 1 of 10 File: PGPB Nov 21, 2002

PGPUB-DOCUMENT-NUMBER: 20020172999
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020172999 A1

TITLE: Novel KIAA1061-like cell adhesion molecule-like proteins and polynucleotides encoding them

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

2. Document ID: US 20020168716 A1

L11: Entry 2 of 10 File: PGPB Nov 14, 2002

PGPUB-DOCUMENT-NUMBER: 20020168716
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020168716 A1

TITLE: Novel amino acid sequences for human microfibril glycoprotein 4-like polypeptides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

3. Document ID: US 20020055141 A1

L11: Entry 3 of 10 File: PGPB May 9, 2002

PGPUB-DOCUMENT-NUMBER: 20020055141
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020055141 A1

TITLE: Corynebacterium glutamicum strain with enhanced secretion activity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

4. Document ID: US 6455253 B1

L11: Entry 4 of 10 File: USPT Sep 24, 2002

US-PAT-NO: 6455253
DOCUMENT-IDENTIFIER: US 6455253 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc
Image

☐ 5. Document ID: US 6406855 B1

L11: Entry 5 of 10 File: USPT Jun 18, 2002

US-PAT-NO: 6406855
DOCUMENT-IDENTIFIER: US 6406855 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc
Image

☐ 6. Document ID: US 6355484 B1

L11: Entry 6 of 10 File: USPT Mar 12, 2002

US-PAT-NO: 6355484
DOCUMENT-IDENTIFIER: US 6355484 B1

TITLE: Methods and compositions for polypeptides engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc
Image

☐ 7. Document ID: US 6335160 B1

L11: Entry 7 of 10 File: USPT Jan 1, 2002

US-PAT-NO: 6335160
DOCUMENT-IDENTIFIER: US 6335160 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 8. Document ID: US 6319713 B1

L11: Entry 8 of 10 File: USPT Nov 20, 2001

US-PAT-NO: 6319713
DOCUMENT-IDENTIFIER: US 6319713 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

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☐ 9. Document ID: US 6303344 B1

L11: Entry 9 of 10 File: USPT Oct 16, 2001

US-PAT-NO: 6303344
DOCUMENT-IDENTIFIER: US 6303344 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

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☐ 10. Document ID: US 6093794 A

L11: Entry 10 of 10 File: USPT Jul 25, 2000

US-PAT-NO: 6093794
DOCUMENT-IDENTIFIER: US 6093794 A

TITLE: Isolated peptides derived from the Epstein-Barr virus containing fusion inhibitory domains

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

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Terms	Documents
L10 and l7	10

Display Format: - Change Format

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WEST

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Search Results - Record(s) 1 through 18 of 18 returned.

☐ 1. Document ID: US 20020172999 A1

L10: Entry 1 of 18 File: PGPB Nov 21, 2002

PGPUB-DOCUMENT-NUMBER: 20020172999
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020172999 A1

TITLE: Novel KIAA1061-like cell adhesion molecule-like proteins and polynucleotides encoding them

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 2. Document ID: US 20020168716 A1

L10: Entry 2 of 18 File: PGPB Nov 14, 2002

PGPUB-DOCUMENT-NUMBER: 20020168716
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020168716 A1

TITLE: Novel amino acid sequences for human microfibril glycoprotein 4-like polypeptides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 3. Document ID: US 20020055141 A1

L10: Entry 3 of 18 File: PGPB May 9, 2002

PGPUB-DOCUMENT-NUMBER: 20020055141
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020055141 A1

TITLE: Corynebacterium glutamicum strain with enhanced secretion activity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 4. Document ID: US 20020051976 A1

L10: Entry 4 of 18 File: PGPB May 2, 2002

PGPUB-DOCUMENT-NUMBER: 20020051976
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020051976 A1

TITLE: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWMC | Draw Desc

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☐ 5. Document ID: US 6479055 B1

L10: Entry 5 of 18 File: USPT Nov 12, 2002

US-PAT-NO: 6479055
DOCUMENT-IDENTIFIER: US 6479055 B1

TITLE: Methods for inhibition of membrane fusion-associated events, including respiratory syncytial virus transmission

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWMC | Draw Desc

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☐ 6. Document ID: US 6455253 B1

L10: Entry 6 of 18 File: USPT Sep 24, 2002

US-PAT-NO: 6455253
DOCUMENT-IDENTIFIER: US 6455253 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWMC | Draw Desc

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☐ 7. Document ID: US 6406855 B1

L10: Entry 7 of 18 File: USPT Jun 18, 2002

US-PAT-NO: 6406855
DOCUMENT-IDENTIFIER: US 6406855 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWMC | Draw Desc

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☐ 8. Document ID: US 6355484 B1

L10: Entry 8 of 18 File: USPT Mar 12, 2002

US-PAT-NO: 6355484

DOCUMENT-IDENTIFIER: US 6355484 B1

TITLE: Methods and compositions for polypeptides engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

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☐ 9. Document ID: US 6335160 B1

L10: Entry 9 of 18 File: USPT Jan 1, 2002

US-PAT-NO: 6335160
DOCUMENT-IDENTIFIER: US 6335160 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

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☐ 10. Document ID: US 6319713 B1

L10: Entry 10 of 18 File: USPT Nov 20, 2001

US-PAT-NO: 6319713
DOCUMENT-IDENTIFIER: US 6319713 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

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☐ 11. Document ID: US 6303344 B1

L10: Entry 11 of 18 File: USPT Oct 16, 2001

US-PAT-NO: 6303344
DOCUMENT-IDENTIFIER: US 6303344 B1

TITLE: Methods and compositions for polypeptide engineering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

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☐ 12. Document ID: US 6228983 B1

L10: Entry 12 of 18 File: USPT May 8, 2001

US-PAT-NO: 6228983
DOCUMENT-IDENTIFIER: US 6228983 B1

TITLE: Human respiratory syncytial virus peptides with antifusogenic and antiviral activities

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw. Desc

☐ 13. Document ID: US 6093794 A

L10: Entry 13 of 18 File: USPT Jul 25, 2000

US-PAT-NO: 6093794
DOCUMENT-IDENTIFIER: US 6093794 A

TITLE: Isolated peptides derived from the Epstein-Barr virus containing fusion inhibitory domains

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw. Desc

☐ 14. Document ID: US 6068973 A

L10: Entry 14 of 18 File: USPT May 30, 2000

US-PAT-NO: 6068973
DOCUMENT-IDENTIFIER: US 6068973 A

TITLE: Methods for inhibition of membrane fusion-associated events, including influenza virus

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw. Desc

☐ 15. Document ID: US 6060065 A

L10: Entry 15 of 18 File: USPT May 9, 2000

US-PAT-NO: 6060065
DOCUMENT-IDENTIFIER: US 6060065 A

TITLE: Compositions for inhibition of membrane fusion-associated events, including influenza virus transmission

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw. Desc

☐ 16. Document ID: US 6054265 A

L10: Entry 16 of 18 File: USPT Apr 25, 2000

US-PAT-NO: 6054265
DOCUMENT-IDENTIFIER: US 6054265 A

TITLE: Screening assays for compounds that inhibit membrane fusion-associated events

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image

KWIC | Draw. Desc

☐ 17. Document ID: US 6017536 A

L10: Entry 17 of 18 File: USPT Jan 25, 2000

US-PAT-NO: 6017536
DOCUMENT-IDENTIFIER: US 6017536 A

TITLE: Simian immunodeficiency virus peptides with antifusogenic and antiviral activities

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image

KWIC | Draw. Desc

☐ 18. Document ID: US 6013263 A

L10: Entry 18 of 18 File: USPT Jan 11, 2000

US-PAT-NO: 6013263
DOCUMENT-IDENTIFIER: US 6013263 A

TITLE: Measles virus peptides with antifusogenic and antiviral activities

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image

KWIC | Draw. Desc

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Terms	Documents
L9 and (dna or cdna or nucleic acid or polynucleotide)	18

Display Format: - Change Format

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     (FILE 'HOME' ENTERED AT 10:57:54 ON 10 DEC 2002)

     FILE 'HCAPLUS' ENTERED AT 10:58:27 ON 10 DEC 2002
L1            54 SEA ABB=ON  PLU=ON  SECF OR (PROTEINS (L) GENE SECF) OR SECF
                 PROTEIN
L2          1286 SEA ABB=ON  PLU=ON  CORYNEBACTERIA OR CORYNEBACTERIA GLUTAMICUM
                  OR (BACTERIA (L) CORYNEFORM)
L3             0 SEA ABB=ON  PLU=ON  1L (L) L2
L4             7 SEA ABB=ON  PLU=ON  L1 (L) (DNA OR CDNA OR NUCLEIC ACID OR
                 POLYNUCLEOTIDE)
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=> d l4 ibib ab 1-7

L4 ANSWER 1 OF 7 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:833536 HCAPLUS
DOCUMENT NUMBER: 135:367763
TITLE: Corynebacterium glutamicum strain with modifications of secD and secF genes resulting in enhanced secretion activity
INVENTOR(S): Berens, Stephan; Kalinowski, Joern; Puehler, Alfred
PATENT ASSIGNEE(S): Degussa A.-G., Germany
SOURCE: PCT Int. Appl., 42 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001085967	A2	20011115	WO 2001-EP4703	20010426
WO 2001085967	A3	20020228		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1156115	A1	20011121	EP 2000-110021	20000512
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
US 2002055141	A1	20020509	US 2001-852053	20010510

PRIORITY APPLN. INFO.: EP 2000-110021 A 20000512
AB The present invention refers to a Corynebacterium glutamicum bacterial strain which natural genes secD and secF are identified, isolated and sequenced for the first time. Genetical modifications of these new genes, concerning gene sequences as well as gene expression, and genetically modified bacterial strain with enhanced secretion are provided, and the use of such bacterial strain for prodn. of desired substances as well as in a reporter system for protein translocation are described. C. glutamicum secD has a size of 1911 bp. The SecD protein possesses six putative transmembrane spanning regions which are similar to Mycobacterium tuberculosis SecD. The extracytoplasmatic loop of the protein reveals much lesser conservation to the mycobacterial SecD protein. C. glutamicum secF consists of 1209 bp, starts five bases after the secD stop codon and its putative Shine-Dalgarno sequence AGGAG is part of secD 3'-end. The SecF protein is similar to M. tuberculosis SecF and its structure resembles the SecD protein.

L4 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:630016 HCAPLUS
DOCUMENT NUMBER: 135:329186
TITLE: Characterization of the low-pH responses of Helicobacter pylori using genomic DNA arrays
AUTHOR(S): Allan, Elaine; Clayton, Christopher L.; McLaren, Alistair; Wallace, Donald M.; Wren, Brendan W.
CORPORATE SOURCE: Pathogen Molecular Biology and Biochemistry Unit, Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, WC1E 7HT, UK
SOURCE: Microbiology (Reading, United Kingdom) (2001), 147(8), 2285-2292
CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Helicobacter pylori is unique among bacterial pathogens in its ability to

persist in the acidic environment of the human stomach. To identify H. pylori genes responsive to low pH, the authors assembled a high-d. array of PCR-amplified random genomic **DNA**. Hybridization of radiolabeled **cDNA** probes, prepd. using total RNA from bacteria exposed to buffer at either pH 4.0 or pH 7.0, allowed both qual. and quant. information on differential gene expression to be obtained. A previously described low-pH-induced gene, cagA, was identified together with several novel genes that may have relevance to the survival and persistence of H. pylori in the gastric environment. These include genes encoding enzymes involved in LPS and phospholipid synthesis and **secF**, encoding a component of the protein export machinery. A hypothetical protein unique to H. pylori (HP0681) was also found to be acid induced. Genes down-regulated at pH 4.0 include those encoding a sugar nucleotide biosynthesis protein, a flagellar protein and an outer-membrane protein. Differential gene expression was confirmed by total RNA slot-blot hybridization.

REFERENCE COUNT: 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:77694 HCAPLUS
DOCUMENT NUMBER: 130:134974
TITLE: Characterization of the Bacillus subtilis secretion factor SecDF and use in enhanced prodn. and secretion of desired heterologous or homologous proteins
INVENTOR(S): Quax, Wilhelmus J.
PATENT ASSIGNEE(S): Genencor International, Inc., USA; Genencor International B.V.
SOURCE: PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9904007	A1	19990128	WO 1998-US14786	19980716
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1003873	A1	20000531	EP 1998-935747	19980715
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
AU 9884931	A1	19990210	AU 1998-84931	19980716
JP 2001510047	T2	20010731	JP 2000-503213	19980716
US 6258563	B1	20010710	US 2000-462844	20000322
US 2002006641	A1	20020117	US 2001-899482	20010705

PRIORITY APPLN. INFO.:

EP 1997-305286	A	19970716
EP 1997-305344	A	19970717
WO 1998-US14786	W	19980716
US 2000-462844	A1	20000322

AB The present invention provides expression vectors, methods and systems for enhanced prodn. and secretion of desired heterologous or homologous proteins in gram-pos. microorganisms using the Bacillus subtilis secretion factor SecDF. The present invention provided the **nucleic acid** and amino acid sequences for the B. subtilis secretion factor SecDF. The B. subtilis secretion factor SecDF, in contrast to the SecD and **SecF** of Escherichia coli, was found to be encoded by one **nucleic acid** sequence (gene secDF). The protein sequence of B. subtilis secretion factor SecDF was found to be identical to the protein sequence found in GenBank Accession AF024506. The membrane topol. of B. subtilis secretion factor SecDF was described and SecDF was shown to be required for efficient secretion of AmyQ.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:422084 HCAPLUS
DOCUMENT NUMBER: 119:22084
TITLE: The promoter of the tgt/sec operon in Escherichia coli is preceded by an upstream activation sequence that contains a high affinity FIS binding site
AUTHOR(S): Slany, Robert K.; Kersten, Helga
CORPORATE SOURCE: Inst. Biochem., Univ. Erlangen-Nuernberg, Erlangen, D-8520, Germany
SOURCE: Nucleic Acids Research (1992), 20(16), 4193-8
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The tgt/s operon in E. coli consists of five genes: queA, tgt, ORF12, secD, and **secF**. QueA and Tgt participate in the biosynthesis of the hypermodified tRNA nucleoside Queuosine, whereas SecD and **SecF** are involved in protein secretion. Examn. of the promoter region of the operon showed structural similarity to promoter regions of the rrn-operons. An upstream activation sequence (UAS) contg. a potential binding site for the factor of inversion stimulation (FIS) was found. Gel retardation assays and DNaseI footprinting indicated, that FIS binds specifically and with high affinity to a site centered at position -58. Binding of FIS caused bending of the **DNA**, as deduced from circular permutation anal. Various 5' deletion mutants of the promoter region were constructed and fused to a lacZ reporter gene to det. the influence of the UAS element on the promoter strength. An approx. two-fold activation of the promoter by the UAS element was obsd.

L4 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:54514 HCAPLUS
DOCUMENT NUMBER: 118:54514
TITLE: Overproduction, purification and characterization of SecD and SecF, integral membrane components of the protein translocation machinery of Escherichia coli
AUTHOR(S): Matsuyama, Shinichi; Fujita, Yasuhiro; Sagara, Kazuhiko; Mizushima, Shoji
CORPORATE SOURCE: Inst. Appl. Microbiol., Univ. Tokyo, Tokyo, 113, Japan
SOURCE: Biochimica et Biophysica Acta (1992), 1122(1), 77-84
CODEN: BBACAQ; ISSN: 0006-3002
DOCUMENT TYPE: Journal
LANGUAGE: English
AB SecD and **SecF proteins** were overproduced by means of recombinant **DNA** technol. Immunoblot and amino-acid sequencing anal. revealed that the overproduced proteins are SecD and **SecF**. The SecD- or **SecF**-overproduced membrane fraction was subjected to differential solubilization. The SecD protein was then purified through ion-exchange and size-exclusion chromatogs. The **SecF protein** was purified through size exclusion chromatog. Proteoliposomes reconstituted from the purified SecD and **SecF** together with SecE and SecY were used to analyze the translocation activity. SecD and **SecF** did not exhibit significant effects on the translocation activity of proteoliposomes. The amts. of SecD and **SecF** in overproducers were detd. densitometrically on a stained SDS gel and their overprodn. (fold) was detd. by means of immunoblot anal. Then the no. of these mols. in one normal cell were estd. From these nos., together with those of other Sec proteins, the no. of translocation apps. existing in one E. coli cell was inferred to be around 500.

L4 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1991:576144 HCAPLUS
DOCUMENT NUMBER: 115:176144
TITLE: Structure and organization of Escherichia coli genes involved in biosynthesis of the deazaguanine derivative queuine, a nutrient factor for eukaryotes
AUTHOR(S): Reuter, Klaus; Slany, Robert; Ullrich, Frank; Kersten, Helga

CORPORATE SOURCE: Inst. Biochem., Univ. Erlangen-Nuernberg, Erlangen, D-8520, Germany
SOURCE: Journal of Bacteriology (1991), 173(7), 2256-64
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The plasmid pPR20 contains the gene tgt, which encodes tRNA guanine transglycosylase (Tgt), on a 33-kbp **DNA** insert from a region around 9 min on the E. coli linkage map. The plasmid was subcloned to det. the sequence and organization of the tgt gene. Tgt is a unique enzyme that exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAs with GU(N) anticodons. After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside gueuosine (Q). Here the complete sequence of a 3545-bp StuI-BamHI **DNA** fragment is given which includes the tgt gene and three previously unknown genes encoding proteins with calcd. mol. masses of 42.5 (Tgt), 14, 39, and 12 kDa. The gene products were characterized on SDS gels after synthesis in a combined transcription-translation system. The mRNA start sites of the open reading frames (ORFs) were detd. by primer extension anal. Plasmids contg. the ORF encoding the 39-kDa protein (ORF 39) complemented a mutation in Q biosynthesis after the Tgt step. This gene was designated queA. The genes are arranged in the following order: ORF 14 (transcribed in the counterclockwise direction), queA, tgt, and ORF 12 (all transcribed in the clockwise direction). The organization of the promoter sequences and the termination sites suggests that queA, tft, and ORF 12 are localized on a putative operon together with the genes secD and **secF**.

L4 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1991:179102 HCAPLUS
DOCUMENT NUMBER: 114:179102
TITLE: The secD locus of E. coli codes for two membrane proteins required for protein export
AUTHOR(S): Gardel, C.; Johnson, K.; Jacq, A.; Beckwith, J.
CORPORATE SOURCE: Dep. Microbiol. Mol. Genet., Harvard Med. Sch., Boston, MA, 02115, USA
SOURCE: EMBO Journal (1990), 9(10), 3209-16
CODEN: EMJODG; ISSN: 0261-4189
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Cold-sensitive mutations in the secD locus of E. coli result in severe defects in protein export at the non-permissive temp. of 23.degree.. **DNA** sequence of a cloned fragment that includes the secD locus reveals open reading frames for 7 polypeptide chains. Both deletions and TnphoA insertions in this clone have been used in maxicell and complementation studies to define the secD locus and its products. The secD mutations fall into two complementation groups, defining genes designated secD and **secF**. These 2 genes comprise an operon, the first case of 2 genes involved in the export process being co-transcribed. The **DNA** sequence of the 2 genes along with alk. phosphatase fusion anal. indicates that they code for integral proteins of the cytoplasmic membrane. These 2 proteins may form a complex in the membrane which acts at late steps in the export process.

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     (FILE 'HOME' ENTERED AT 10:46:41 ON 10 DEC 2002)

     FILE 'HCAPLUS' ENTERED AT 10:46:46 ON 10 DEC 2002
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L2          1286 SEA ABB=ON  PLU=ON  CORYNEBACTERIA OR CORYNEBACTERIA GLUTAMICUM
                  OR (BACTERIA (L) CORYNEFORM)
L3             0 SEA ABB=ON  PLU=ON  L1 (L) L2
L4            14 SEA ABB=ON  PLU=ON  L1 (L) (DNA OR CDNA OR NUCLEIC ACID OR
                 POLYNUCLEOTIDE)
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L4 ANSWER 1 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:539792 HCAPLUS
DOCUMENT NUMBER: 137:104741
TITLE: Gene sequences from Methylococcus capsulatus as probes in DNA arrays for the determination of differential gene expression
INVENTOR(S): Birkeland, Nils Kare; Eidhammer, Ingvar; Jonassen, Inge; Jensen, Harald B.; Lien, Torleiv; Lillehaug, Johan R.; Lossius, Ivar; Eisen, Jonathan A.; Fraser, Claire M.; Durkin, A. Scott; Salzberg, Steven L.
PATENT ASSIGNEE(S): Unifob, Stiftelsen Universitetsforskning I Bergen, Norway; TIGR
SOURCE: PCT Int. Appl., 678 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002055655	A2	20020718	WO 2002-NO19	20020114

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: NO 2001-235 A 20010112
NO 2001-239 A 20010112

AB The invention related to method and systems for the detn. of alteration of gene expression in Methylococcus capsulatus under a variety of conditions. A preferred embodiment of the invention relates to microarrays comprising polynucleotides or oligonucleotides representative for a selective no. of the genes of M. capsulatus. Thus, whole genome random sequencing and assembly of M. capsulatus strain NCIMB 11132 was achieved with a total of 6- and 2-fold coverage of genome from BMC and BMD plasmid libraries. The genes are used as probes for the generation of an array system for the detn. of differential expression due to alterations in incubation conditions, for example, at high or low concns. of Cu2+. Subsets of DNA sequences are identified for measurement of key metabolic features (metab. of C and N, serine and butanediol pathways, lipid metab., and energy metab.), regulator genes, and transport and secretion. The sequences for a total of 1840 DNA fragments and/or genes of M. capsulatus are provided.

L4 ANSWER 2 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:833536 HCAPLUS
DOCUMENT NUMBER: 135:367763
TITLE: Corynebacterium glutamicum strain with modifications of secD and secF genes resulting in enhanced secretion activity
INVENTOR(S): Berens, Stephan; Kalinowski, Joern; Puehler, Alfred
PATENT ASSIGNEE(S): Degussa A.-G., Germany
SOURCE: PCT Int. Appl., 42 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001085967	A2	20011115	WO 2001-EP4703	20010426

WO 2001085967 A3 20020228
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 1156115 A1 20011121 EP 2000-110021 20000512
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
US 2002055141 A1 20020509 US 2001-852053 20010510
PRIORITY APPLN. INFO.: EP 2000-110021 A 20000512

AB The present invention refers to a Corynebacterium glutamicum bacterial strain which natural genes secD and secF are identified, isolated and sequenced for the first time. Genetical modifications of these new genes, concerning gene sequences as well as gene expression, and genetically modified bacterial strain with enhanced secretion are provided, and the use of such bacterial strain for prodn. of desired substances as well as in a reporter system for protein translocation are described. C. glutamicum secD has a size of 1911 bp. The SecD protein possesses six putative transmembrane spanning regions which are similar to Mycobacterium tuberculosis SecD. The extracytoplasmatic loop of the protein reveals much lesser conservation to the mycobacterial SecD protein. C. glutamicum secF consists of 1209 bp, starts five bases after the secD stop codon and its putative Shine-Dalgarno sequence AGGAG is part of secD 3'-end. The SecF protein is similar to M. tuberculosis SecF and its structure resembles the SecD protein.

L4 ANSWER 3 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:258302 HCAPLUS
DOCUMENT NUMBER: 134:350561
TITLE: Enterotoxin production and other characteristics of Staphylococcus aureus strains isolated from human nasal carriers
AUTHOR(S): Stephan, R.; Senczek, D.; Dorigoni, V.
CORPORATE SOURCE: Institute for Food Safety and Hygiene, University of Zurich, Zurich, CH-8057, Switz.
SOURCE: Archiv fuer Lebensmittelhygiene (2001), 52(1), 7-9
CODEN: ALMHAO; ISSN: 0003-925X
PUBLISHER: Verlag M. & H. Schaper GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Staphylococcus aureus strains obtained from nasal swabs of healthy carriers were identified and further characterized by pheno- and genotypic methods. This included the identification of staphylococcal enterotoxin (SE) types, antibiotic resistance testing, the appraisal of hemolysis, the egg yolk reaction, the detection of the clumping factor, and protein A by latex agglutination, the PCR amplification of a species specific part of the 23S rRNA-gene, the PCR amplification of the coagulase (coa) gene, and a macrorestriction anal. of the chromosomal **DNA**. Within the 13 strains, there were 6 SED-, 2 SEAD-, and 1 **SECD**-formers. Eleven of the 13 strains were resistant to penicillin G/ampicillin. PCR amplification of the 3' end of the coa gene showed 4 different sized amplicons within the 13 strains. Macrorestriction anal. revealed 11 PFGE patterns.

REFERENCE COUNT: 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:653084 HCAPLUS
DOCUMENT NUMBER: 134:143067
TITLE: Cloning,expression and characteristics of disintegrin-like/cysteine-rich domains cDNA from Agkistrodon acutus venom
AUTHOR(S): Liu, Qing-du; Zhang, Jia-lin; Cheng, Xin; Liu, Ai-ping; Liu, Jing

CORPORATE SOURCE: School of Life Sciences, University of Science and Technology of China, Hefei, 230027, Peop. Rep. China
SOURCE: Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao (2000), 16(4), 462-467
CODEN: ZSHXF2; ISSN: 1007-7626
PUBLISHER: Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao Bianweihui
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
AB By means of RT-PCR, a **cDNA** gene was obtained from the total RNA of Agkistrodon acutus venom. The clone was 964 bp in length,which encoded a complete open reading frame of 216 amino acid residues. The **cDNA**-deduced amino acid sequence was rich in cysteines and highly similar to jararhagin-C and catrocollastatin-C of Bothrops jararaca. The Arg-Gly-Asp(RGD) tripeptide sequence found in disintegrin was replaced by Ser-Gly-Cys-Asp (**SECD**) in the disintegrin-like domain. The recombinant disintegrin-like/cysteine-rich domains were expressed as a fusion protein with glutathione S-transferase in E. coli and the recombinant protein was an inhibitor of the collagen-induced but not ADP-induced platelet aggregation.

L4 ANSWER 5 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:772969 HCAPLUS
DOCUMENT NUMBER: 132:118206
TITLE: Taurine modulates expression of transporters in rat brain and heart
AUTHOR(S): Labudova, O.; Yeghiazarjan, C.; Hoger, H.; Lubec, Gert
CORPORATE SOURCE: Dep. Pediatrics, Univ. Vienna, Vienna, A-1090, Austria
SOURCE: Amino Acids (1999), 17(3), 301-313
CODEN: AACIE6; ISSN: 0939-4451
PUBLISHER: Springer-Verlag Wien
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In pro- and eucaryotic life, cellular and subcellular compartments are sepd. by membranes and the regulated and selective passage of specific mols. across these membranes is a basic and highly conserved principle. The authors were interested whether taurine, a naturally occurring amino acid, would be able to induce or suppress expression of transporters with the rationale that taurine was shown to detoxify a series of endogenous toxins and xenobiotics of various chem. non-related structures. For this purpose the authors used a gene hunting technique, subtractive hybridization, subtracting mRNAs of taurine-treated rat brain and heart from untreated controls. Subtracted mRNAs were then converted to **cDNAs**, amplified, sequenced and identified by gene bank data. The authors found 5 transporter transcripts, the phosphonate transport ATPase PHNC, multidrug transporter homolog MTH104, protein-export-membrane protein **SECD**, oligopeptide transporters oppA and oppD, in the brain and two: ABC-transporter BRAF-2 and cation-transport ATPase PACS, in the heart. Homologies of the sequences found were in any case >50% thus permitting the identification of transporters with high probability. The biol. meaning could be that a naturally occurring amino acid, taurine, modulates complex transport systems. The most prominent finding is the upregulation of a multidrug transporter transcript, explaining a mechanism for the nonselective detoxifying action of taurine.
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 6 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:77694 HCAPLUS
DOCUMENT NUMBER: 130:134974
TITLE: Characterization of the Bacillus subtilis secretion factor SecDF and use in enhanced prodn. and secretion of desired heterologous or homologous proteins
INVENTOR(S): Quax, Wilhelmus J.
PATENT ASSIGNEE(S): Genencor International, Inc., USA; Genencor International B.V.
SOURCE: PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9904007	A1	19990128	WO 1998-US14786	19980716
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1003873	A1	20000531	EP 1998-935747	19980715
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
AU 9884931	A1	19990210	AU 1998-84931	19980716
JP 2001510047	T2	20010731	JP 2000-503213	19980716
US 6258563	B1	20010710	US 2000-462844	20000322
US 2002006641	A1	20020117	US 2001-899482	20010705

PRIORITY APPLN. INFO.:
EP 1997-305286 A 19970716
EP 1997-305344 A 19970717
WO 1998-US14786 W 19980716
US 2000-462844 A1 20000322

AB The present invention provides expression vectors, methods and systems for enhanced prodn. and secretion of desired heterologous or homologous proteins in gram-pos. microorganisms using the Bacillus subtilis secretion factor SecDF. The present invention provided the **nucleic acid** and amino acid sequences for the B. subtilis secretion factor SecDF. The B. subtilis secretion factor SecDF, in contrast to the **SecD** and SecF of Escherichia coli, was found to be encoded by one **nucleic acid** sequence (gene secDF). The protein sequence of B. subtilis secretion factor SecDF was found to be identical to the protein sequence found in GenBank Accession AF024506. The membrane topol. of B. subtilis secretion factor SecDF was described and SecDF was shown to be required for efficient secretion of AmyQ.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 7 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:784270 HCAPLUS
DOCUMENT NUMBER: 130:137956
TITLE: Cloning and sequencing of yajC and secD homologs of Brucella abortus and demonstration of immune responses to YajC in mice vaccinated with B. abortus RB51
AUTHOR(S): Vemulapalli, Ramesh; Duncan, A. Jane; Boyle, Stephen M.; Sriranganathan, Nammalwar; Toth, Thomas E.; Schurig, Gerhardt G.
CORPORATE SOURCE: Center for Molecular Medicine and Infectious Diseases, Department of Biomedical Sciences and Pathobiology, VA-MD Regional College of Veterinary Medicine, Virginia Polytechnic Institute and State University, Blacksburg, VA, 24061-0342, USA
SOURCE: Infection and Immunity (1998), 66(12), 5684-5691
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To identify Brucella antigens that are potentially involved in stimulating a protective cell-mediated immune response, a gene library of Brucella abortus 2308 was screened for the expression of antigens reacting with IgG2a antibodies from BALB/c mice vaccinated with B. abortus RB51. One selected pos. clone (clone MBP68) contained an insert of 2.6 kb; nucleotide sequence anal. of this insert revealed two open reading frames (ORFs). The deduced amino acid sequences of the first and second ORFs had significant similarities with the YajC and SecD proteins, resp., of several bacterial species. Both the YajC and SecD proteins were expressed

in Escherichia coli as fusion proteins with maltose binding protein (MBP). In Western blots, sera from mice vaccinated with B. abortus RB51 recognized YajC but not SecD. Further Western blot anal. with purified recombinant YajC protein indicated that mice inoculated with B. abortus 19 or 2308 or B. melitensis RM1 also produced antibodies to YajC. In response to in vitro stimulation with recombinant MBP-YajC fusion protein, splenocytes from mice vaccinated with B. abortus RB51 were able to proliferate and produce gamma interferon but not interleukin-4. This study demonstrates, for the first time, the involvement of YajC protein in an immune response to an infectious agent.

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 8 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:758058 HCAPLUS
DOCUMENT NUMBER: 128:86339
TITLE: Genetic basis of the MbrC "ploidy" phenotype in Escherichia coli
AUTHOR(S): Estevenon, A.-M.; Lemonnier, M.; Rouquette, C.; Lane, D.
CORPORATE SOURCE: Lab. Microbiologie Genetique Moleculaire, CNRS, Toulouse, F-31062, Fr.
SOURCE: Molecular & General Genetics (1997), 256(3), 291-297
CODEN: MGGEAE; ISSN: 0026-8925
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The mbrC17 mutation in Escherichia coli had been shown to cause conditional growth defects and an increase in the quantity of **DNA** per cell. The present work was aimed at identifying the mutation. Sequencing showed that the MbrC17 phenotype does not involve glr (murI), as previously suggested. P1 transduction data indicated that the mbrC17 mutation is closely linked to rpoB, and allele exchange showed it to lie within the **secD**-nusG operon. A single change relative to wild type was found in the secE-nusG region from the mbrC17 strain, a G .fwdarw. A mutation 23 bp upstream of the secE coding sequence. This mutation causes a two-fold increase in the concn. of secE-nusG mRNA.

L4 ANSWER 9 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:537193 HCAPLUS
DOCUMENT NUMBER: 123:190932
TITLE: Molecular cloning and expression of catrocollastatin, a snake-venom protein from Crotalus atrox (eastern diamondback rattlesnake) which inhibits platelet adhesion to collagen
AUTHOR(S): Zhou, Qing; Smith, J. Bryan; Grossman, Mark H.
CORPORATE SOURCE: Dep. Pharmacology, Temple Univ. Sch. med., Philadelphia, PA, 19140, USA
SOURCE: Biochemical Journal (1995), 307(2), 411-17
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A 50 kDa protein that inhibits platelet adhesion to collagen has been isolated from snake venom of Crotalus atrox (western diamondback rattlesnake) and has been named 'catrocollastatin'. The **cDNA** cloning of catrocollastatin has been accomplished. A full-length **cDNA** of 2310 bp with an open reading frame between nucleotides 51 and 1880 was obtained. The deduced amino acid sequence consists of 609 amino acids. The **cDNA**-predicted amino acid sequence is highly similar to that of hemorrhagic metalloproteinase jararhagin from Bothrops jararaca venom, HR1B from Trimeresurus flavoviridis, Ht-e from C. atrox and trigamin from T. gramineus. Like jararhagin and HR1B, catrocollastatin is a multidomain mol. composed of an N-terminal domain, a metalloproteinase domain, a disintegrin-like domain and a cysteine-rich C-terminal domain. In the disintegrin-like domain, the frequently seen RGD (Arg-Gly-Asp) sequence is replaced by **SECD** (Ser-Glu-Cys-Asp). This **cDNA** was expressed in Spodoptera frugiperda (fall armyworm) (Sf9) insect cells using a baculovirus

expression system. Like native catrocollastatin, the expressed protein is capable of selectively blocking collagen-induced platelet aggregation. This is the first full-length clone of a high-mol.-mass hemorrhagin to be expressed.

L4 ANSWER 10 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:422084 HCAPLUS
DOCUMENT NUMBER: 119:22084
TITLE: The promoter of the tgt/sec operon in Escherichia coli is preceded by an upstream activation sequence that contains a high affinity FIS binding site
AUTHOR(S): Slany, Robert K.; Kersten, Helga
CORPORATE SOURCE: Inst. Biochem., Univ. Erlangen-Nuernberg, Erlangen, D-8520, Germany
SOURCE: Nucleic Acids Research (1992), 20(16), 4193-8
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The tgt/s operon in E. coli consists of five genes: queA, tgt, ORF12, **secD**, and secF. QueA and Tgt participate in the biosynthesis of the hypermodified tRNA nucleoside Queuosine, whereas **SecD** and SecF are involved in protein secretion. Examn. of the promoter region of the operon showed structural similarity to promoter regions of the rrn-operons. An upstream activation sequence (UAS) contg. a potential binding site for the factor of inversion stimulation (FIS) was found. Gel retardation assays and DNaseI footprinting indicated, that FIS binds specifically and with high affinity to a site centered at position -58. Binding of FIS caused bending of the **DNA**, as deduced from circular permutation anal. Various 5' deletion mutants of the promoter region were constructed and fused to a lacZ reporter gene to det. the influence of the UAS element on the promoter strength. An approx. two-fold activation of the promoter by the UAS element was obsd.

L4 ANSWER 11 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:54514 HCAPLUS
DOCUMENT NUMBER: 118:54514
TITLE: Overproduction, purification and characterization of SecD and SecF, integral membrane components of the protein translocation machinery of Escherichia coli
AUTHOR(S): Matsuyama, Shinichi; Fujita, Yasuhiro; Sagara, Kazuhiko; Mizushima, Shoji
CORPORATE SOURCE: Inst. Appl. Microbiol., Univ. Tokyo, Tokyo, 113, Japan
SOURCE: Biochimica et Biophysica Acta (1992), 1122(1), 77-84
CODEN: BBACAQ; ISSN: 0006-3002
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **SecD** and SecF proteins were overproduced by means of recombinant **DNA** technol. Immunoblot and amino-acid sequencing anal. revealed that the overproduced proteins are **SecD** and SecF. The **SecD**- or SecF-overproduced membrane fraction was subjected to differential solubilization. The **SecD protein** was then purified through ion-exchange and size-exclusion chromatogs. The SecF protein was purified through size exclusion chromatog. Proteoliposomes reconstituted from the purified **SecD** and SecF together with SecE and SecY were used to analyze the translocation activity. **SecD** and SecF did not exhibit significant effects on the translocation activity of proteoliposomes. The amts. of **SecD** and SecF in overproducers were detd. densitometrically on a stained SDS gel and their overprodn. (fold) was detd. by means of immunoblot anal. Then the no. of these mols. in one normal cell were estd. From these nos., together with those of other Sec proteins, the no. of translocation apps. existing in one E. coli cell was inferred to be around 500.

L4 ANSWER 12 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1991:576144 HCAPLUS
DOCUMENT NUMBER: 115:176144
TITLE: Structure and organization of Escherichia coli genes involved in biosynthesis of the deazaguanine derivative queuine, a nutrient factor for eukaryotes

AUTHOR(S): Reuter, Klaus; Slany, Robert; Ullrich, Frank; Kersten, Helga
CORPORATE SOURCE: Inst. Biochem., Univ. Erlangen-Nuernberg, Erlangen, D-8520, Germany
SOURCE: Journal of Bacteriology (1991), 173(7), 2256-64
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The plasmid pPR20 contains the gene tgt, which encodes tRNA guanine transglycosylase (Tgt), on a 33-kbp **DNA** insert from a region around 9 min on the E. coli linkage map. The plasmid was subcloned to det. the sequence and organization of the tgt gene. Tgt is a unique enzyme that exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAs with GU(N) anticodons. After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside gueuosine (Q). Here the complete sequence of a 3545-bp StuI-BamHI **DNA** fragment is given which includes the tgt gene and three previously unknown genes encoding **proteins** with calcd. mol. masses of 42.5 (Tgt), 14, 39, and 12 kDa. The gene products were characterized on SDS gels after synthesis in a combined transcription-translation system. The mRNA start sites of the open reading frames (ORFs) were detd. by primer extension anal. Plasmids contg. the ORF encoding the 39-kDa protein (ORF 39) complemented a mutation in Q biosynthesis after the Tgt step. This gene was designated queA. The genes are arranged in the following order: ORF 14 (transcribed in the counterclockwise direction), queA, tgt, and ORF 12 (all transcribed in the clockwise direction). The organization of the promoter sequences and the termination sites suggests that queA, tft, and ORF 12 are localized on a putative operon together with the **genes** **secD** and secF.

L4 ANSWER 13 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1991:179102 HCAPLUS
DOCUMENT NUMBER: 114:179102
TITLE: The secD locus of E. coli codes for two membrane proteins required for protein export
AUTHOR(S): Gardel, C.; Johnson, K.; Jacq, A.; Beckwith, J.
CORPORATE SOURCE: Dep. Microbiol. Mol. Genet., Harvard Med. Sch., Boston, MA, 02115, USA
SOURCE: EMBO Journal (1990), 9(10), 3209-16
CODEN: EMJODG; ISSN: 0261-4189
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Cold-sensitive mutations in the **secD** locus of E. coli result in severe defects in protein export at the non-permissive temp. of 23.degree.. **DNA** sequence of a cloned fragment that includes the **secD** locus reveals open reading frames for 7 polypeptide chains. Both deletions and TnphoA insertions in this clone have been used in maxicell and complementation studies to define the **secD** locus and its products. The **secD** mutations fall into two complementation groups, defining genes designated **secD** and secF. These 2 genes comprise an operon, the first case of 2 genes involved in the export process being co-transcribed. The **DNA** sequence of the 2 genes along with alk. phosphatase fusion anal. indicates that they code for integral proteins of the cytoplasmic membrane. These 2 proteins may form a complex in the membrane which acts at late steps in the export process.

L4 ANSWER 14 OF 14 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1990:113003 HCAPLUS
DOCUMENT NUMBER: 112:113003
TITLE: The secE gene encodes an integral membrane protein required for protein export in Escherichia coli
AUTHOR(S): Schatz, Peter J.; Riggs, Paul D.; Jacq, Annick; Fath, Michael J.; Beckwith, Jon
CORPORATE SOURCE: Dep. Microbiol. Mol. Genet., Harvard Med. Sch., Boston, MA, 02115, USA
SOURCE: Genes & Development (1989), 3(7), 1035-44
CODEN: GEDEEP; ISSN: 0890-9369

DOCUMENT TYPE: Journal
LANGUAGE: English

AB Genetic screening and selection procedures employing a secA-lacZ fusion strain repeatedly have yielded mutations in 4 genes affecting the protein export pathway of E. coli. These genes are secA, **secD**, prlA/secY, and secE. The significance of the failure to find new sec genes after extensive use of this approach is discussed. One of the genes, secE, has been characterized in some detail. The **DNA** sequence of the gene and anal. of alk. phosphatase fusions to the SecE protein indicate that it is a 13,600-dalton integral cytoplasmic membrane protein. Apparently, secE has an important role in E. coli protein export.